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Title: •
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein -
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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             protein search, using sw model
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/Dackfiles1.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               June 21, 2001, 10:43:57; Search time 11.68 Seconds (without alignments) 115.556 Million cell updates/sec
              \begin{array}{c} \Sigma_1 \\ \Sigma_2 \\ \Sigma_3 \\ \Sigma_4 \\ \Sigma_5 
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Gapop 10.0 , Gapext 0.5
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                  DB
    US-08-276-967-2
US-08-465-380-59
US-08-486-397-59
US-08-486-399-59
US-08-486-399-59
US-08-634-641-59
US-09-249-471-59
US-09-249-451-59
US-09-249-461-59
US-09-249-461-59
US-08-486-399-128
US-08-486-399-128
US-08-486-399-128
US-08-486-399-128
US-08-486-391-128
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US-09-249-471-128
US-09-249-471-128
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Sequence 2, Appli Sequence 59, Appl Sequence 128, Appl Sequ
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Prot. Leng Inde	Sequence Seq	Query Match 27.5%; Score 107.5; Dest Local Similarity 33.3%; Pred. No. 0.002 Matches 22; Conservative 9; Mismatches	SYSTEM: PC-DOS/MS-DOS PATENTIN Release #1.0, Version PATRICULATION DATA: ON NUMBER: US/08/276,967 TE: Submitted Herewith ATION: 530 ENT INFORMATION: ttchell, Barbara S. FION NUMBER: UTSD:418\KIT CCATION INFORMATION: 1713-787-1400 713-787-1400 713-789-2679 90-924 ON SEG ID NO: 2: LARACTERISTICS: 2476 amino acids lino acid ESS: Single Linear TPE: protein	David L. Species-Specific Egg- Sperm Sperm	-08 -486 - 397 -49 -08 -486 - 399 -25 -08 -486 - 399 -25 -08 -481 -965 -25 -08 -461 -965 -25 -08 -461 -25 -08 -634 -641 -25 -08 -634 -641 -25 -09 -249 -471 -25 -09 -249 -472 -25 -09 -249 -472 -25 -09 -249 -451 -25 -09 -249 -451 -25 -08 -809 -455 -25 -08 -809 -455 -45 -08 -809 -455 -45
S-08-466-397-49 5-08-466-399-25 5-08-461-965-25 5-08-461-965-25 5-08-634-641-25 5-08-634-641-25 5-09-249-471-25 5-09-249-472-25 5-09-249-472-25 5-09-249-451-25 5-09-249-451-25 5-09-249-451-25 5-09-249-451-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-08-809-455-25 5-09-249-471-25 8-8110, Version #1.25 Prot. DB 2: Leng Pro	S-08-486-397-49 Sequence 5-08-486-399-25 Sequence 5-08-461-965-25 Sequence 5-08-461-965-49 Sequence 5-08-634-641-25 Sequence 5-08-634-641-25 Sequence 5-09-249-471-25 Sequence 5-09-249-471-25 Sequence 5-09-249-472-25 Sequence 5-09-249-451-25 Sequence 5-08-809-455-25 Sequence 5-09-249-451-25 Seque	27.5% 33.3% tive	PC-DOS IIn Relea I DATA: RE US/C RE US/C RMATION: Barbara Barbara Barbara Barbara Barbara BRR: 33 RUMBER: RMFORMATI RMFORMATI RFORMATI	Daniel M David David Specie Sperm Sperm SeESS: d, White	00000000000000000
86-397-49 86-397-49 86-399-25 86-399-25 86-399-25 86-399-49 261-965-25 49-4710-54 34-641-25 49-471-25 49-471-25 49-471-25 49-451-25 09-455-25 09-455-25 09-455-25 107.5; DB 2; Leng NNC. 0.0028; Inde	86-397-49 86-397-49 86-399-25 Sequence 9-471-49 Sequence 9-471-25 Sequence 49-471-25 Sequence 49-451-25 Sequence 9-455-25 Sequence 9-455-49 Version #1.25 Version #1.25 Version #1.25 Version #1.25 Ino. 0.0028; Indels 17;	Sco Pre 9;	#1.0 #1.0 276,9 ewith 8 8 TSD:4		11111111111111
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Sequence	uence	DB 2 028; 18	#1. 2	Binding	9595959595559595
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US-08-465-380-59
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                                                                                                                                          Matches
                                                                                                                                                       Query Match .25.68;
Best Local Similarity 30.48;
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                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yves R. Laroche
APPLICANT: Yannick G.J. Gar
APPLICANT: Peter W. Bergum
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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STREET: Suite 4700
CITY: Los Apport
                                                                                                      11 KCPSNEIFSRCDGR~CQRFC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 21
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62 DKCVSAEDC 70
                                  58 KVCVPRSKC 66
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                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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California
                                                                                                                                                                                                                                                                                                                                    84 amino acids
                                                                                                                                        Conservative
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Joris H.L. Mensens, Marc J. Lauwereys,
Yves R. Laroche, Laurent S. Jespers,
Yannick G.J. Gansemans, Matthew Moyle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
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                                                                                                                                      Score 100; DB 2; Length 84
Pred. No. 0.00071;
8; Mismatches 24; Indels
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                                                                                                    ---PNVVPKPLCIKICAPGCVCRLGYLRNKK 57
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                                               US-08-486-399-59
                                                                   RESULT
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US-08-486-397-59
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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Sequence 59, Applicat Patent No. 5866543 GENERAL INFORMATION:
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Best Local Similarity 30.4
Matches 21; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 499-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yannick G.
APPLICANT: Peter W. E
TITLE OF INVENTION: N
TITLE OF INVENTION: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
LENGTH: 84 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/486,397 FILING DATE: June 5, 1995
                                                                                                                                                                                    62 DKCVSAEDC
                                                                                                                                                                                                                            58 KVCVPRSKC
                                                                                                                                                                                                                                                                                                          11 KCPSNEIFSRCDGR-CQRFC-------PNVVPKPLCIKICAPGCVCRLGYLRNKK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e 59, AFE
NO. 5866542
                                                           9, Application US/08486399
5866543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 amino acids
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George P. Vlasuk, Patric H. Joris H.L. Mensens, Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ancyclostoma caninum
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                                                                                                                                                                                                                                                                                                                                                                   25.6%;
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                                                                                                                                                                                                                                                                                                                                                                   Score 100; DB 2; Length 84; Pred. No. 0.00071;
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                                                                                                                                                                                                                                                                                                                                                   Mismatches
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RESULT 5
US-08-461-965-59
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                                                                                                                                                        Patent No. 5872098
GENERAL INFORMATION:
                                                                                                                                                                                                Sequence 59,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/326,110
APPLICATION NUMBER: 0ctober 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                APPLICANT: George P. Vlasuk, Patric H.
APPLICANT: Joris H.L. Mensens, Marc J.
APPLICANT: Yves R. Laroche, Laurent S.
APPLICANT: Yannick G.J. Gansemans, Matt
APPLICANT: Peter W. Bergum
                                TITLE OF INVENTION: NEMĀTODE-EXTRACTED ANTICOAGULANT TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Anc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DALL. 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
08/326,110
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                         62 DKCVSAEDC 70
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TENGTH: 84 a..._
Tinear
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CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                           QCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNV----PCLVRVCHQDCVCEEGFYRNKD 63
                                                                                                                                                                                                Application US/08461965
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Pred. No. 0.00071;
Pred. No. 24; Indels
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                                                                                   Matthew Moyle,
                                                                                                                                           Stanssens,
                                                                                                                        Lauwereys,
                                                                                                         Jespers
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US-08-461-965-59
                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                              Sequence 59, Application US/08634641 Patent No. 5955294
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Best Local Similarity
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                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                           APPLICANT:
                                                  CORRESPONDENCE ADDRESS:
                                                                             APPLICANT: Bergum, Peter W.
TITLE OF INVENTION: NEMATOD
TITLE OF INVENTION: PROTEIN
                                                                                                                                               APPLICANT:
APPLICANT:
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ORIGINAL SOURCE:
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FILLING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/24
                                                                 NUMBER OF SEQUENCES:
                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                  ADDRESSEE:
STREET: 6
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                             62 DKCVSAEDC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08 FILING DATE: June 5, 1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                           58 KVCVPRSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 KCPSNEIFSRCDGR-CQRFC------PNVVPKPLCIKICAPGCVCRLGYLRNKK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           5 QCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNV---PCLVRVCHQDCVCEEGFYRNKD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                         Vlasuk, George P. Vlasuk
Stanssens, Patrick Eric Hugo
Mensens, Joris Hilda Lieven
                                                                                                                                                             Laroche, Yves Rene
Jespers, Laurent Stephane
                                                                                                                                              Gansemans, Yannick Georges Jozef
                                                                                                                              Moyle, Matthew
                                                                                                                                                                                             Lauwereys,
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                                                                                  PROTEIN
                                                                                                  NEMATODE-EXTRACTED ANTICOAGULANT
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                                                                 356
                                                                                                                                                                                               Marc Josef
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                                                                                                                                                                                           Sequence 5 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Anc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: OCTOBER 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
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MEDIUM TYPE: 3.5" Di:
MEDIUM TYPE: storage
              APPLICANT:
                                                                    APPLICANT:
APPLICANT:
                                                                                                      APPLICANT:
APPLICANT:
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LENGTH: 84 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/326.110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                 62 DKCVSAEDC 70
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6040441
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California
F: Bergum, Peter W.
INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
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                                                                                                                      Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                      Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
                                  Moyle, Matthew
                                                       Gansemans,
                                                                    Jespers, Laurent Stephane
                                                                                    Laroche, Yves Rene
                                                                                                      Lauwereys, Marc Josef
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UMBER: 08/326,110
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                                                     Yannick Georges Jozef
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Pred. No. 0.00071;
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Sequence 59, Application US/09249472 Patent No. 6046318 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION UNMBER: 30,158
REFERENCE/DOCKET NUMBER: 216,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/132:
APPLICATION NUMBER: PCT/US95/132:
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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LENGTH: 84 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                        11 KCPSNEIFSRCDGR-CQRFC-------PNVVPKPLCIKICAPGCVCRLGYLRNKK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: April
                                                                                                                                       62 DKCVSAEDC 70
                                                                                                                                                                           58 KVCVPRSKC
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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633 West Fifth Street
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(213) 955-0440
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17, 1997
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APPLICANT: Vlasuk, George Phillip

Gaps

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62 DKCVSAEDC 70

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US-09-249-472-59
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                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/809,455
FILING DATE: APril 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
APPLICATION NUMBER: 08/326,110
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
ORGANISM: And
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                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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STREET: 633 West Fifth Street
STREET: Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BIGGS, SUZANN REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                        11 KCPSNEIFSRCDGR-CQRFC------PNVVPKPLCIKICAPGCVCRLGYLRNKK 57
                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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   58 KYCVPRSKC 66
                                                                                                                                Local Similarity
                                     QCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNV---PCLVRVCHQDCVCEEGFYRNKD 61
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Jespers, Laurent Stephane
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Messens, Joris Hilda Lieven
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                                                                                                                 Conservative
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                                                                                                                                                                                                                                                             peptide
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                                                                                                                   8; Mismatches
                                                                                                                            Score 100; אם ב.
No. 0.00071;
                                                                                                                                                        DB 3; Length 84;
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US-09-249-451-59
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US-09-249-451-59
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
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APPLICANT:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US95/132
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
FILING DATE: June 5, 1995
FILING DATE: June 5, 1995
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MEDIUM TYPE: 3.5" Dis
MEDIUM TYPE: storage
COMPUTER: IBM Compati
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                                                                                                                                                                                                                                        FILING DATE: October 18, ATTORNEY/AGENT INFORMATION: NAME: BIGGS, SUZANNE L. REGISTRATION NUMBER: 30,
                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                        FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
                  ORGANISM:
                                                                     TOPOLOGY:
                                                                                    TYPE: amino acids
                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
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Messens, Joris Hilda Lieven
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Moyle, Matthew
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Jespers, Laurent Stephane
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                    Ancyclostoma caninum
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US-08-809-455-59

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INFORMATION FOR SEQ ID NO:
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                               SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
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APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
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APPLICATION NUMBER: US/08/809,455
FILING DATE: April 17, 1997
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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                 TOPOLOGY: linear
                                                                                                    TELEFAX: (213) 955-0440
TELEX: 67-3510
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APPLICATION NUMBER: 08/**-.
TING DATE: June 5, 1995
TING DATE: 08/326,110
                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
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STREET: 633 West Fifth Street
STREET: Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90071
                                                                                                                                                                                               BIGGS, SUZANNE L
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laroche,
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Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jespers, Laurent Stephane
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                                                                                                                                (213) 489-1600
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8; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                         APPLICATION NUMBER: 08/486,399
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5,1995
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                                             FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ANTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                 FILING DATE: April APPLICATION NUMBER: FILING DATE: Octobe
REFERENCE/DOCKET NUMBER:
                                    NAME:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
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Jespers, Laurent Stephane
Cangemans, Yannick Georges Jozef
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Messens, Joris Hilda Lieven
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                                                                                                                                                                                   October 17, 17, 1990
NUMBER: 08/486,399
                        SUZANNE L.
                                                                                                                                                                                                                                                               April 17,
                                                                                                                                                                                                                                                                                                                                                                                     IBM P.C.
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               30,158
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216/270
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Pred. No. 0.00071;
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ZIP:

COUNTRY:

NAME:

TELEPHONE:

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; MOLECULE TYPE: p
; ORIGINAL SOURCE:
; ORGANIŚM: Ancy
US-09-249-461-59
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Best Local Similarity
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
           APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                       ZIP: 900/1
COMPUTER READABLE FORM:
VENTUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                       SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Tonne
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CORRESPONDENCE ADDRESS:
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TYPE: amino acid
TYPE: linear
TYPE: location
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
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APPLICATION NUMBER:
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Jespers, Laurent Stephane
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                                                                                                                                                                                                                                                            IBM P.C.
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Pred. No. 0.00071;
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; Patent No. 5863894
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Best Local S
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5
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APPLICANT:
                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yannick G.J. Gar
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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LENGTH: 84 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                            STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Log 2-
                                                                                                                                                                       SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                         COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                            STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                        APPLICATION NUMBER: 08/326,110
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APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 QCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNV---PCLVRVCHQDCVCEEGFYRNKD 61
                                                                                                                                                                                                                                                                                           90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 amino acids
                                                                                                                                                                                                                                                                                                           U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       George P. Vlasuk, Patric H. Stanssens,
Joris H.L. Mensens, Marc J. Lauwereys,
Yves R. Laroche, Laurent S. Jespers,
Yannick G.J. Gansemans, Matthew Moyle,
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                                                                                                                                                                                                           IBM Compatible
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JMBER: 08/461,965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN
                                                                                                                                                                                             IBM P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50,
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Best Local Similarity
Matches (21; Conserv
                                                 FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: 18 OCTOBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
PEFERENCE/DOCKET NUMBER: 208/290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GEORGE P. VLASUK; PATRICK ERIC APPLICANT: HUGO STANSSENS; JORIS HILDA APPLICANT: LIEVEN MESSENS; MARC JOZEF APPLICANT: LAUWEREYS; YVES RENE LAROCHE; APPLICANT: LAURENT STEPHANE JESPERS; and APPLICANT: YANNICK GEORGES JOZEF APPLICANT: GANSEMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
                 TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTITITLE OF INVENTION: COAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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TELEX: 67-3510
                                                                                                                                                                                                                                                                               COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 KVCVPRSKC 66
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                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/480,478
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TELÉFAX:
               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Lyon & Lyon
633 West Fifth Street
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(213) 955-0440
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                                                                                                                                                                                                                                                                                 IBM P.C.
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                                                                                                                                                                                                                                                                                   DOS 5.0
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Best Local Similarity
Watches 21; Conserve
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ORGANISM:
US-08-486-397-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 128, Application US/08486397 Patent No. 5866542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 91 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 128:
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: LOS Anna?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/486,397 FILING DATE: June 5, 1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 QCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNV---PCLVRVCHQDCVCEEGFYRNKD 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                          TOPOLOGY:
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                                                                                          amino acid
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California
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                 Ancyclostoma caninum
                                                                          linear
                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN: 357
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                           Result
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                 107.5
104.5
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(without alignments)
239.824 Million cell updates/sec
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391
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Gapop 10.0 , Gapext 0.5
 93435 seqs, 34255486 residues
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                                                                                                                                                                                                                                                                                                                                   Length DB
                                                                                                                                                                                              2813
937
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1416
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ANCIPIA
VWE_CANFA
VWE_BOVIN
A62F_DOMM
A62F_DOMMO
BAR3_CHITE
ICEL_ASCSU
YOJZ_CAEEL
IGIR_RAT
IGIR_MOUSE
ICEZ_ASCSU
MT11_MYTED
ST14_MOUSE
VC2_HUMAN
TSP3_MOUSE
TENX_HUMAN
MT_PERFL
VT81_WYAN
IGIR_HUMAN
IGIR_HUMAN
IGIR_HUMAN
IGIR_HUMAN
IGIR_HUMAN
IGIR_HUMAN
IGIR_HUMAN
IGIR_HUMAN
TENA_PIG
ITR1_ASCSU
MT12_MYTED
MTB_ONCMY
MT_ESOLU
FPIF_BOMMO
ERB3_RAT
MT14_MYTED
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                                                                                                                                                                                                                                    Q28295 canis famil
P80012 bos taurus
O46202 drosophila
P04275 homo sapien
Q28833 sus scrofa
P98092 bombyx mori
Q03376 chironomus
  p49746 homo sapien
p08069 homo sapien
Q29116 sus scrofa
p19398 ascaris suu
p80247 mytilus edu
p09862 oncorhynchu
p25127 esox lucius
Q10731 bombyx mori
Q62799 rattus norv
p80249 mytilus edu
                                                                                                p07851 ascaris suu
p34625 caenorhabdi
p24062 rattus norv
Q60751 mus musculu
p07852 ascaris suu
p80246 mytilus edu
p56677 mus musculu
p34015 variola vir
Q02817 homo sapien
Q05895 mus musculu
p22105 homo sapien
p52725 perca fluvi
Q03610 caenorhabdi
p29825 myxoma yiru
                                                                                                                                                                                                                                                                                                        Q28983 sus scrofa
P56682 apis mellif
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                                                                                       7 homo sapien
5 mus musculu
5 homo sapien
5 perca fluvi
0 caenorhabdi
5 myxoma viru
6 homo sapien
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InterPro;

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MBL; 040024; AAC48486.1; interPro; IPR000561; interPro; IPR000998; interPro; IPR001846; interPro; IPR002919;	his SWISS-PROT entry is copyright. It is produsetween the Swiss Institute of Bioinformatics he European Bioinformatics Institute. There as see by non-profit institutions as long as isolated and this statement is not removed. Usentities requires a license agreement (See http. r send an email to license@isb-sib.ch).	OLIGOMENTALIST CONTAINS 1 MAM DOMAIN. - SIMILARITY: CONTAINS 4.5 VWFD DOMAINS. - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.	ADHESION TO !- DOMAIN: DUI THE MUCIN SPERMATOZO. !- DOMAIN: TH		1. Chem. 270:26025-26028(1995). NCTION: BINDS IN A SPECIES-SPEC THE EGG.	JENCE FROM N.A. ALNa-MEJISHAN; TISSUE=Testis; LINE=96064658; PubMed=7592795 dy D.M., Garbers D.L.; dy D.M. Garbers D.L.; sperm membrane protein that begg extracellular matrix is tor.":	ofa (Pi ca; Met h; Euth (ID=982	028983; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) 20NADHESIN PRECURSOR.	1 G AN_PIG STANDARD; PRT; 2476 AA.	ALIGNMENTS	68 17.4 60 1 MT_PLEPL 68 17.4 60 1 MT_PEEPL 68 17.4 4660 1 LRP2_RAT 67 17.1 318 1 KRUC_SHEEP 67 17.1 325 1 YRP1_CAEEL 68 17.1 325 1 YRP1_CHMAN 69 17.1 525 1 YRP1_CHMAN 69 17.1 325 1 YRP1_CHMAN 60 17.1 1 TENA_SHEEP 61 17.1 2911 1 KR2A_SHEEP 62 17.0 17.1 1 KR2A_SHEEP 63 17.0 400 1 PRTZ_HUMAN 64 15.9 16.9 1 MTB_SALSA 65 15.0 60 1 MTB_SALSA 65 16.9 780 1 DCMA_METTH 65 17.0 salmo salar 66 16.9 10 1 DCMA_METTH 67 17.1 1 KR2A_SHEEP 68 17.0 400 1 PRTZ_HUMAN 69 18 18 18 18 18 18 18 18 18 18 18 18 18

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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS50060; MAM_2; 2.
15-JUL-1999 (Rel. 38, Created)
30-MAY-2000 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CHYMOTRYPSIN INHIBITOR (AMCI).
Apis mellifera (Honeybee).
Ekkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Meoptera; Endopterygota; Hymenoptera; Apocrita; Acc
Apoidea; Apidae; Apis.
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Pred. No. 0.00079;
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O1-OCT-2000 (Rel. 40, Las
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Best Local
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Wancuso D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;
"The canine von Willebrand factor gene: sequence and expression c
a region encoding the glycoprotein ID/IX binding domain.";
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases:
- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEDSTASIS, IT
PARTICIPATES IN PLATTELET-VESSEL WALL INTERACTIONS BY FORMING
NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE
VASCULAR INJURY (BY SIMILARITY).
-1- SUBUNIT: MULTIMERIC (BY SIMILARITY).
                                                                                                                                                                                   "Venta P.J., Li J., Yuzbasiyan-Gurkan V., Brewer G.J., Sch
"Complete sequence of the structural gene for canine von
factor and identification of a mutation causing Scottish
Willebrand's disease.";
                                                                                                                                                                                                                      SEQUENCE FROM N.A. Venta P.J., Li J.,
                                                                                                                                                                                                                                                             Montgomery R.R., Fahs S., Mc
Submitted (AUG-1996) to the
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                                                                                                                                           SEQUENCE OF 1234-1669 FROM N.A.
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                                                                                                                                                                                                                                                                                                                  Submitted
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Canis familiaris (Dog).
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"Primary structure and properties of the cathepsin G/chymotrypsin inhibitor from the larval hemolymph of Apis mellifera.";
Eur. J. Blochem. 262:680-687(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Hemolymph;
MEDLINE=99339935; PubMed=10411628;
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SEQUENCE, AND STRUCTURE BY
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he EMBL/GenBank/DDBJ databases
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Pfam; PF00007; Cys.knot; 1.
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Pfam; PF00093; vwc; 3.
Pfam; PF00093; vwc; 3.
Pfam; PF00094; vwd; 4.
PRINTS; PF00453; VWFADONAIN.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01295; CTCK_2; 1.
PROSITE; PS01206; VWFA; 3.
PROSITE; PS01206; VWFC; 3.
PROSITE; PS012106; VWFC; 3.
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EMBL; L16903; AAA30903.1; --
EMBL; AF099154; AAD04919.1; --
EMBL; U66246; AAB93766.1; --
HSSP; P04275; LATZ.
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P80012; Q28011;
01-NOV-1995 (Rel. 32, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
VON WILLEBRAND FACTOR PRECURSOR (VWF) (FRAGMENT).
F8VWF OR VWF.
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MEDLINE=97307751; PubMed=9165093;
Janel N., Ribba A.S., Cherel G.,
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NCBI_TaxID=9913;
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Mammalia; Eutheria;
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PROSITE; PS01225; CTCK_2; PARTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of factor-XIIIa-reactive glutaminyl residues propolypeptide of bovine von Willebrand factor."; Eur. J. Biochem. 232:773-777(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91192039; PubMed-1707363; Fujisawa T., Takagi J., Sekiya F., Goto A., Fujisawa T. antibodies that inhibit binding "Monoclonal antibodies"
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gloden K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIson D.R., Nelson K.A., Nurphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                     A62F_DROME
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BERKELEY;

MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

George R.A., Lewis S.E., Richards S., Ashburner M., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhange M., Pfeiffer B.D.,

Miklos G.L.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wolfner M.F., Harada H.A., Bertram M.J., Stelick T.J., Kraus Kalb J.M., Lung Y.O., Neubaum D.M., Park M., Tram U.K.; "New genes for male accessory gland proteins in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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01-0CT-2000
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CARBOHYD
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MISSING (IN REF. 3).
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Pred. No. 0.0016;
Pred. No. 0.0016;
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Shue B.C.,
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01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
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EMBL; AE003475; AAF47683.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                            Mancuso D.J., Tuley E.A., Westfield L.A., Worrall N.K., Shelton-Inloes B.B., Sorace J.M., Alevy Y.G., Sadler J. "Structure of the gene for human von Willebrand factor. J. Biol. Chem. 264:19514-19527(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F8VWF OR VWF.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90062044; PubMed=2584182;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
  TISSUE-Umbilical vein endothelial cells;
                                                                                                                                                            Bonthron D., Orr E.C., Mitsock L.M.,
                                                                                                                                                                                               MEDLINE-87016349;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                  Nucleic Acids
                                SEQUENCE OF 1-120 FROM N.A.,
                                                                                                               "Nucleotide sequence
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14:7125-7128(1986).
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MEDLINE-87213253; PubMed-3495266; Shelton-Inloes B.B., Broze G.J. Jr., Miletich J.P., Sadler J.E.; "Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated domains, and relationship to von Willebr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verweij
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MEDLINE=85201687;
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Morin M.J., Dombalagian M.J., Ricca G
Lynch D.C.;
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                                                                                                                                                                                                                                                                                                        MEDLINE=93356762;
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MEDLINE=91185602; F
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PubMed=8352759;
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PROSITE; PS01208; VWFA; 3.

PROSITE; PS01108; VWFC; 3.

PROSITE; PS01185; CTCK_1; 1.

PROSITE; PS01125; CTCK_2; 1.

PROSITE; PS01225; CTCK_2; 1.

Blood coagulation; Platelet; Glycoprotein; Extracellular matrix;

Prosite; Ps0121; Repeat; Cell adhesion.
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KOTANI E., IWAMOTO S.I., TASHITO M., MORI H., SUMIDA M., MATSUBARA F., YAMAKAWA M.; SUBMITTAN (JAN-1993) TO THE EMBL/GENBANK/DDBJ DATABASES.
-!- FUNCTION: ADHESIVE PROTEIN AND RELAYES TO HEMOSTASIS ENCAPSULATION OF FOREIGN SUBSTANCES FOR SELF-DEFENSE.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN HEMOCYTES DURING LA
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01-FEB-1996 (Rel. 33, Last sequence u
01-NOV-1997 (Rel. 35, Last annotation
HEMOCYTIN PRECURSOR (HUMORAL LECTIN).
Bombyx mori (Silk moth).
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-FUYOU X TOKAI; TISSUE-Hemocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
                                                                                                                                                                                                                                                                                                                    Kotani E., Yamakawa M., Iwamoto S.-I., Tashiro
Matsubara F., Taniai K., Kadono-Okuda K., Kato
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95178544; PubMed=7873598;
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SIMILARITY: THE N-TERMINAL DOMAIN SHOWS SOME SIMILARITY TO THAT
                                                             OR VIRAL INFECTION AND INHIBITED GALACTOSAMINE AND D-MALTOSE.
                                                                                             INDUCTION: HEMAGGLUTINATION
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19; Conserv
                                             MAY BE CONVERTED INTO THE 260 KDA MATURE HEMOCYTIN
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InterPro; IPRO01846; ...
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InterPro; IPRO02919; ...
Pfam; PF00754; F5_F8_type_C; 2
Pfam; PF001826; TIL; 6
Pfam; PF001826; TIL; 6
Pfam; PF001826; TIL; 6
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Pfam; PF001826; CTCK_1; 1.
PROSITE; PS01208; VWFC; FALSE_I
PROSITE; PS01208; FAS8C_1; 2.
PROSITE; PS01286; FAS8C_1; 2.
PROSITE; PS01286; FAS8C_2; 2.
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SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 2 VWFC DOMAINS.
SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
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Q03376;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea; Chironomidae; Chironominae; Chironomus.

NCBI_TaxID=7153;
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                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation updat
BALBIANI RING PROTEIN 3 PRECURSOR.
                  PIR; S08167; S08167.
HSSP; P18055; 2MRB.
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         InterPro;
                                        EMBL; X52263; CAA36506.1;
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                                                                                                                                              SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: SALIVARY GLAND.
DOMAIN: HAS 82 APPROXIMATE REPEATS OF CYS-X-CYS-X-CYS.
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PRINTS; PR00876; MINEMATODE

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DISULFID 17 29
DISULFID 21 60
DISULFID 40 54
ACT_SITE 31 32
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SIGNAL
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01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
CHYMOTRYPSIN/ELASTASE ISOINHIBHTOR 1 (C/E-1 INHIBHTOR).
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
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P07851;
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Pfam; PF01826; TIL; 1
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IPASQC
                                                          GQESCGPNEVWTECTGCEMKCGPDENTPCPLMCRRPSC--ECSPG----RGMRRTNDGKC 54
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                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               BELONGS TO THE
                                                                                                                                                                                              6862 MW;
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                                                                                                                               20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186145 MW;
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                                                                                                                     10;
                                                                                                                                                                                                                                                                                                      3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
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Pred.
                                                                                                                  Score 80.5; DB pred. No. 0.031; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BALBIANI RING PROTEIN 3.
fW; 34202B28521B0815 CRC64;
                                                                                                                                                                                             REACTIVE BOND.
5DC10DE75B375F16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                  ASCARIS TRYPSIN INHIBITOR FAMILY.
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                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ascaris
                                                                                                                                                Length 63;
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RESULT 1
IG1R_RAT
ID IG1R
AC P240
DT 01-W
DT 01-W
DT 01-C
DE INSU
GN IGF1
OS RATT
OC Mamm
OX NCB:
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YOJ2_CAEEL
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Best Local
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopne S., Shownkeen I
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditidae; Pel
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YOJ2_CAEEL
                                                                           01-MAR-1992 (Rel. 21, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation updat
INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECU
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. SEQUENCE 99 AA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterson R., Watson Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                            P24062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L15313; AAA28199.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "2.2 Mb of contiguous nucleotide sequence from chromosome
elegans.";
                                               Rattus norvegicus (Rat).
                                                                IGF1R
                                                                                                                                                          G1R_RAT
                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                    44 PGCV 47
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                                                                                                                                                                                                                                      AGCV
                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZK353.2; CE00386.
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(Rel. 28, Last sequence update)
(Rel. 29, Last annotation update)
L 10.6 KDA PROTEIN ZK353.2 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 10561 MW;
                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                               20.6%;
                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                  Score 80.5; DB Pred. No. 0.043;
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                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                 862C659838E47E5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                update)
PRECURSOR
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                                                                                (EC
                                                                                                                                                                                                                                                                                                                                                                                                 Length 99;
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Pfam;
Pfam;
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                                                                                                            PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00239; RECEPTOR TYR KIN_II; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kidney.";
Biochem. Biophys. Res. Commun. 187:934-939(1992).
-i- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT TYROSINE-PROTEIN KINASE ACTIVITY.
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
    DOMAIÑ
                                CHAIN
                                                                                                                                                                        PRINTS; PR00109;
                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                   Transferase;
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                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA."; circ. Res. 76:963-972(1995).
                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                      interPro;
                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92412145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 913-1017 FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leroith D.; "Developmental regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90017496; PubMed=2477843;
Werner H., Woloschak M., Adamo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 1-364 FROM N.A.
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Du J., Delafontair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A new member
                                                                                                                                                                                           erPro; IPR000494; -.
erPro; IPR000719; -.
erPro; IPR001245; -.
erPro; IPR001777; -.
erPro; IPR002011; -.
erPro; IPR0020114; -.
erPro; IPR0020116; -.
erPro; IPR0020116; -.
erPro; IPR0020116; -.
erPro; IPR00041; fn; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LICAND-BINDING DOWAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                            ; L29232; AAA41392.1; ...
; M27293; AAA41384.1; ...
A33837; A33837.
; P06213; 1IRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                  PF00041;
PF00069;
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                                                                                                                                                                                                                                                                                                                                                                                                               requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene."
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                                                                                                Tyrosine-protein kinase; Receptor;
                                                                                   ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A.
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                                                                                                                                                                                  pkinase; 1.
                                                                                                                                                                     TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K., Ohta M., Kawasaki T., Itoh N.;
the insulin receptor family, insulin
receptor, is expressed preferentially
                              1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1530648;
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    936
                                                                                  Phosphorylation;
                BETA-CHAIN
                          ALPHA-CHAIN.
INSULIN-LIKE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the rat insulin-like growth factor I
EXTRACELLULAR (POTENTIAL)
                                                         INSULIN-LIKE
                                                                       POTENTIAL.
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                                                                                               Transmembrane;
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                             FACTOR
                                                      FACTOR I RECEPTOR.
                                                                                  Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
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Best Local
                                                                                                                                   SEQUENCE OF 1-329 ENC.
STRAIN-CD-1; TISSUE-Kidney;
Jun W., Liu Z., Alvares K., K
Submitted (NOV-1993) to the F
                                                                                                                                                                                                                                                                                        Navarro M., Gazza
"Cloning of cDNA f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGIR_MOUSE STANDARD; PRT; 1373 AA 060751; 062123; 070438; 01-NOV-1997 (Rel. 35, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation updat INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECU
SEQUENCE OF 1134-1203 FROM N.A. MEDLINE=90152381; PubMed=2482828; Wilks A.F., Kurban R.R., Hovens C.M., Ral "The application of the polymerase chain of the protein tyrosine kinase family."; Gene 85:67-74(1989).
                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PRINTS; PR00109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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EMBL; M33422; AAA40013.1;
HSSP; P11362; 1FGI.
MGD; MGI:96433; Igflr.
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                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN EUropean Bioinformatics Institute. There are no restrictly pron-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGA BINDING DOMAIN, WHILE THE BETA CHAIN CARRIES THE KINASE DOMAIN, SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I) WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A TYROSINE-PROTEIN KINASE ACTIVITY.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
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FIBRONECTIN TYPE-III.
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01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
                                                                                                                                                                                              InterPro; IPR002919; Pfam; PF01826; TIL; 1
                                                                                                                                                                                                                                      lumbricoides: the primary structure.";
Arch. Biochem. Biophys. 232:143-161(1984).
-!- FUNCTION: DEFEND THE ORGANISM AGAINST THE HOST'S PROTEINASES
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                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                      MEDLINE=84255715; PubMed=6564898;
                                                                                                                                                                                                                                                                 "The isoinhibitors of chymotrypsin/elastase from
                                                                                                                                                                                                                                                                                                                                                                                                         ICE2
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MISSING (IN INHIBITOR 2).
K -> E (IN INHIBITOR 3).
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                  Score 78.5; D
Pred. No. 0.05
6; Mismatches
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C -> S (IN REF. 2)
D -> G (IN REF. 2)
D -> G (IN REF. 2)
C -> V (IN REF. 2)
C -> S (IN REF. 2)
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C -> S (IN REF. 3)
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                             e 78.5; DB 1;
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RKPCGKNEVWTECTG-CELKCGQDEKTPCALMCRPPSCECTPGRGMRRTHDGKCVPVSEC

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MTIL_MYTED

ID MTIL_M
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DT 01-FEB
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RA MECHAN
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Search completed: June 21, 2001, 10:52:57 Job time: 145 sec
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RX MEDLINE-94062828; PubMed-8243463;
RA Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
RA Mackay E.A., Overnell J.E.;
RA Kaegi J.H.R., Fothergill J.E.;
RY "Complete amino acid sequences of five dimeric and four monomeric
RY "Complete amino acid sequences of five dimeric and four monomeric
RY Torms of metallothionein from the edible mussel Mytilus edulis.";
RE LUT. Biochem. 218:183-1944(1993).
C: I. J. Biochem. 218:183-1944(1993).
C: I. SUBUNIT: MONOMER.
C: SUBUNIT: MONOMER.
C: SUBUNIT: MONOMER.
C: INDUCTION: BY CADMIUM.
C: SIMILARITY: BELONGS TO FAMILY 2 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR: S39416, S39416.
DR PIR: S39416, S39416.
DR PIR: S39416; S39416.
DR PIR: S19416; S19416.
DR PIR: S19416.
DR PIR
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Best Local Similarity 37.2
Matches 16; Conservative
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MT11_MYTED STANDARD; . PRT; 72 AA.

P80246;
P80246;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-WOV-1997 (Rel. 35, Last annotation update)
METALLOTHIONEIN 10-I (MT-10-I).

MYT1lus edulis (Blue mussel).

Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloidea; Mytiloidea; Mytilus.
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391 .
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thrombospondin 3 ~	mucin 2 precursor,	otogelin - mouse	gene G4R protein -	G2R protein - vari	hypothetical prote	hypothetical prote	hypothetical prote	metallothionein 10	hypothetical prote	hypothetical prote	hypothetical prote	chymotrypsin/elast	hypothetical prote	integumentary muci	hypothetical prote

ALIGNMENTS

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-561 <WILL>
                                                                                                                                                                                                                                                                                                             hypothetical protein Y69H2.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Introns: 61/1; 83/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F32D8.3
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A;Residues: 1-245 <WIL>
A;Cross-references: EMBL;Z74031; PIDN:CAA98455.1; GSPDB:GN00023; CESP:F32D8.3
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R;Wilkinson, J.
A; Gene: CESP:Y69H2.3a
                           C; Genetics
                                                  A;Cross-references: EMBL:Z98877; PIDN:CAB54472.1; GSPDB:GN00023; CESP:Y69H2.3a
A;Experimental source: clone Y69H2
                                                                                                                                                                                     A; Reference number: A; Accession: T27318
                                                                                                                                                                                                              submitted to the EMBL Data Library, August 1997 A; Reference number: Z20343
                                                                                                                                                                                                                                                                R; McMurray, A.
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Matches 28
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112 CPRTK 116
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Pred. No. 3.4e-06;
7; Mismatches 20;
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R;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P. J. Biol. Chem. 272, 8791-8801, 1997
A;Title: The mouse tectorins. Modular matrix proteins A;Reference number: 220771; MUID:97236843
A;Accession: T30197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha tectorin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T30197
RESULT
T42215
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A; Residues: 1-626 <WIL>
A; Cross-references: EMBL; Z98877; PIDN: CAB54473.1;
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                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X99805; NID:g1915908; PIDN:CAA68138.1; PID:g1915909 A;Experimental source: strain CD1; whole cochleae A;Note: non-collagenous protein only expressed in the inner ear, by cells bo
                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-2155 <LEG>
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A; Introns: 183/1; 247/1; 312/1; 353/1; 383/1; 429/1; 453/2; 522/1; 546/2;
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A; Accession: T27319
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C;Accession: T27319
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A;Introns: 183/1; 247/1; 288/1; 318/1; 364/1; 388/2; 457/1; 481/2; 521/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 CPVNEVSNECHNPCTEKKCPQKNAPQVNCLMACQVGCSCMDGFVRNNQGVCVKEAEC 179
                                                                                 983 ECPENSHFEEC-MTCTETCETLALGPICVDSCSEGCQCDEGY-RLQGSQCVTRSECG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watch 30.2%; Score 118; DB 2; J
Local Similarity 36.8%; Pred. No. 0.0002;
Comparative 11; Mismatches 23;
                                                                                                                          11 KCPSNEIFSRCDGRCQRFCPNVVPKPLCIKICAPGCVCRLGYLRNKKKVCVPRSKCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 CPSNEIFSRCDGRC-QRFCPNV-VPKPLCIKICAPGCVCRLGYLRNKKKVCVPRSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 CPSNEIFSRCDGRC-QRECPNV-VPKPLCIKICAPGCVCRLGYLRNKKKVCVPRSKC 66
                                                                                                                                                                                        Local Similarity
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                     G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                      Conservative
                                                                                                                                                                                        28.9%;
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                                                                                                                                                                                        Score 113; DB 2; Length 2155; Pred. No. 0.0016;
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPDB:GN00023; CESP:Y69H2.3b
                                                                                                                                                                        26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 561;
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                                                                                                                                                                        Indels
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C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T42215
                                                                                                                                                                                              В
                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: Zan
                                                                                                             T24294
                                                                                                                                 RESULT
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                                                                                                                                                                                              82
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                                                                                                                                                                                                                                                                                 23;
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R;Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A;Title: Species diversity in the structure of zonadhesin,
A;Reference number: 222080; MUID:98123114
A;Accession: T42215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zonadhesin - mouse
N;Alternate names: sperm-specific membrane protein
N;Alternate names: sperm-specific membrane protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
hypothetical protein T01D3.3b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T24294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:T01D3.3a
A; Map position: 5
A; Introns: 74/1; 121/1; 200/2; 493/1; 673/3; 772/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, October 1996 A; Reference number: Z19870 A; Accession: T24293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T01D3.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Residues: 1-5376 <GAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: clone T01D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:281110; PIDN:CAB03259.1; GSPDB:GN00023; CESP:T01D3.3a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-802 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4743 KCPANSLYTHCLPTCLPSCSN--PDGRCEGTSHKAPSTCREGCVCQPGYLLN-KDTCVHK 4799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 KCPSNEIFSRCDGRCQRFCPNVVPKPLC-----IKICAPGCVCRLGYLRNKKKVCVPR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                   12 CPSNEIFSRCDGRCQRFCPNVVPKPLC-IKICAPGCVCRLGYLR---NKKKVCVPRSKC 66
                                                                                                                                                                                                                                  CGANEQYSACFSSCQPSCQD-PSTPACPAPGCQPGCICLPGYIRRDSSPRSACVPRGLC 139
                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Score 109.5;
Pred. No. 0.0
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Pred. No. 0.0031;
8; Mismatches 22; Indels 1
                                                                                                                                                                                                                                                                                                                                             0.0017;
ches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 802;
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د.
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R:Hardy, D.M.; Garbers, D.L.
J. Biol. Chem. 270, 26025-26028, 1995
A;Title: A sperm membrane protein that binds
A;Reference number: Z21464; MUID:96064658
A;Accession: T34022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP:T01D3.3b
A; Map position: 5
A; Introns: 74/1; 126/1
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A;Molecule type: DNA
A;Residues: 1-949 <WIL>
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A;Residues: 1-2476 <HARP>
A;Cross-references: EMBL:U40024; NID:g1066465; PID:g1066466; PIDN:AAC48486.1
A;Experimental source: strain Meishan; testis
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                                                                                              submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C25E10.
A;Reference number: 218376
A;Accession: T15609
                                                                                                                                                                                                                 hypothetical protein C25E10.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15609
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C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
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                        A; Molecule type: DNA
A; Residues: 1-137 <BRA>
                                                                                                                                                                                             R;Bradshaw, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:U50311; NID:g1226295; PID:g1226303; PIDN:AAA92313.1; CESP:C25E:
                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                              1507 PLSQCG 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 CGANEQYSACFSSCQPSCQD-PSTPACPAPGCQPGCICLPGYIRRDSSPRSACVPRGLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 27.5%;
Local Similarity 33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 PRSKCG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 KCPSNEIFSRCDGRC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QRFCPNVVPKPLCIKICAPGCVCRLGYLRNKKKVCV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 107.5; DB Pred. No. 0.006;
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C; Genetics:
A; Gene: CESP: C25E10.8
A; Introns: 1/3; 19/1; 42/3
                                                                                                                             R;Bonthron, D.; Orkin, S.H.

Eur. J. Blochem. 171, 51-57, 1988
A;Title: The human von Willebrand factor gene.
A;Reference number: S02377; MUID:88111704
A;Accession: S02377
                                                                                                                                                                                                                                                                                                                                           von Willebrand factor precursor - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 04-Dec-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 (C;Accession: A34480; S02377; A37139; S23676; A25298; A25469; A25366; S23618; S23645; C;Accession: A34480; S02377; A37139; S23676; Accession: A34480; S02377; A37139; S23676; Accession: A34480; MUID:90062044 A;Accession: A34480; MUID:90062044 A;Accession: A34480; MUID:90062044 A;Accession: A34480; MUID:90062044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein K05F1.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T16574
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A;Cross-references: EMBL:X06828
R;Mancuso, D.J.; Tuley, E.A.; W
Biochemistry 30, 253-269, 1991
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A; Introns: 31/3; 77/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U29377; NID:9868173; PID:9868180; PIDN:AAA68717.1; CESP:K05FA;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-140 <WOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-2813 <MAN>
A; Cross-references: EMBL: M25864
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                                                                              A; Molecule type: DNA
A; Residues: 1-177 <BO2>
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Best Local Similarity 36.8%;
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Best Local Similarity
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                           Westfield, L.A.; Lester-Mancuso,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches
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Pred. No. 0.0034;
7; Mismatches 26;
                                                                                                                                                                                          Structure
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A; Molecule type: mRN/A
A; Residues: 781-788, 'A, 790-1424 <SHE>
A; Note: 852-Gln, 857-Asp, and 1381-Thr were al
R; Ginsburg, D.; Handin, R.I.; Bonthron, D.T.;
Science 228, 1401-1406, 1985
                                                                            A; Reference number: A44178; MUID:85244588 A; Accession: A44178
                                                                                                                                  A; Title: Human von Willebrand factor (vWF):
                                                                                                                                                                                                                                                                                                                                                                                            R; Shelton-Inloes, B.B.; Titani, I
Biochemistry 25, 3164-3171, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 'WA ,739 /C',744-769,'H',771-788,'A',790-803,'S',805-873;1289-1471,'D',1473 A; Note: the authors translated the codon TCG for residue 2168 as Cys R; Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985 A;Title: Cloning and Characterization of two cDNAs coding A;Reference number: A94060; MUID:86016708 A;Accession: A94060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Sadler, J.E.; Shelton-Inloes, B.B.; Proc. Natl. Acad. Sci. U.S.A. 82, 6394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Verweij, C.L.; Diergaarde, P.J.; Hart, M. EMBO J. 5, 1839-1847, 1986
A; Title: Full-length von Willebrand factor A; Reference number: A91044; MUID:87004550
A; Accession: A25469
                                                                                                                                                                                                                                                                                                             A; Accession: A90504
                                                                                                                                                                                                                                                                                                                                           A; Reference number: A90504; MUID: 86269894
                                                                                                                                                                                                                                                                                                                                                                       A; Title: cDNA sequences for
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R;Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.
Biochem. Biophys. Res. Commun. 144, 657-665, 1987
A;Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB.M60675; NID:g340357; PIDN:AAA61295.1; PID:g553810 A;Note: the authors translated the codon CGC for residue 156 as Gln R;Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987 A;Title: Molecular cloning of the human gene for von Willebrand factor and A;Reference number: S23676; MUID:87260814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S23645
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EMBO J. 5, 3074, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X04146
A;Note: this sequence has been revised in reference A91056
R;Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-470,'V',472-483,'R',485-1022,'K',1024-1025,'E',1027-1400
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A; Residues: 1-470, 'V'
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R;Bonthron, D.; Orr, E.C.; Mitsock, L.M.; Ginsburg, D.; Handin, R.I Nucleic Acids Res. 14, 7125-7127, 1986
A;Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA. A;Reference number: A25298; MUID:87016349
A;Accession: A25298
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A;Accession: A37139
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A; Residues: 2731-2813 <COL>
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A; Residues: 990-1947 <MAD>
Molecule type: mknn
Posidues: 2621-2813 <GIN>
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                                                                                                                                                                                                                                                                                                                                                                       human von Willebrand
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                                                                                                                               isolation of complementary DNA (cDNA)
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                                                                                                                                                                                   T.A.; Bruns, G.A.P.; Latt,
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A; Residues: 2731-2813 <LYN>
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A; Residues: 2731-2813
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F;866-1241/Domain: type D repeat 3 <DD3>
F;1275-1443/Domain: von Willebrand factor ty
F;1496-1654/Domain: von Willebrand factor ty
F;1496-1654/Domain: von Willebrand factor ty
F;1689-1854/Domain: von Willebrand factor ty
F;1947-2295/Domain: type D repeat 4 <DD4>
F;296-2330/Domain: type B repeat 1 <VB1>
F;2375-2399/Domain: type B repeat 2 <VB2>
F;2375-2399/Domain: type B repeat 3 <VB3>
F;2430-2497/Domain: von Willebrand factor ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:119125; OMIM:193400

A:Map position: 12p13.3-12p13.2

A;Introns: 19/1; 74/1; 108/2; 178/1; 219/3; 292/1; 333/1; 370/2; 386/1; 431/3; 4

5/1; 1724/1; 1771/1; 1819/1; 1874/1; 1888/3; 1948/1; 2021/3; 2086/1; 2200/1; 226

C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homoloc

C;Keywords: blood coagulation; cell binding; connective tissue; disulfide bond;

F;1-22/Domain: signal sequence #status predicted <SIG>
F;3-763/Product: von Willebrand antigen II #status predicted <WAl>
F;34-386/Domain: type D repeat 1 <DD1>
F;34-386/Domain: type D repeat 1 <DD1>
                                                                                                                                                                                                                                                                                            F;784-865/Domain: D' <DDD>
F;788-833,2216-2261/Region: duplication
F;8826-853,2400-2515,2544-2662/Region: duplication
F;842-1130,1934-2203/Region: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;387-745/Domain: type D repeat 2 <DD2>F;698-700/Region: cell attachment (R-G-D)
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A;Residues: 1606-1617 CBN>
A;Residues: 1606-1617 CBN>
R;Fay, P.J; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B. Science 232, 995-998, 1986
Science 232, 995-998, 1986
A;Title: Propolypeptide of von Willebrand factor circulates in blood and is identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Dent, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
A;Title: Identification of a cleavage site directing the immunochemi
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A;Molecule type: protein
A;Residues: 764-788, 'A', 790-1471, 'D',1473-2813 <TIT>A;Note: 789-Thr was also found
R;Chopek, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.I
Biochemistry 25, 3146-3155, 1986
A;Title: Human von Willebrand factor: a multivalent |
                                                                                                                                                                                                                                                                                                                                                                                                                        F;764-2813/Product: von Willebrand factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A36013; MUID: 90349604
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R;Titani, K.; Kumar, S.; Takio, K.; Ericssc
Biochemistry 25, 317-3184, 1986
A;Title: Amino acid sequences of human von
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A; Residues: 764-773; 2803-2813 <CHO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nd factor: a multivalent protein composed MUID:86269892
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                                                                                                                                                                                                  <VWA2>
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homology <VWC1>

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66 616

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F;2507-2509/Region: cell attachment (R-G-D) motif
F;2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>
F;2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>
F;857,1231,1515,1574,2223,2290,2357,2400,2546,2585,2790/Binding site: carbohydrate (Asn)
F;1147/Binding site: carbohydrate (Asn) (covalent) #status atypical
F;1248,1255,1256,1468,1477,1487,1679,2298/Binding site: carbohydrate (Thr) (covalent) #sf1263,1486/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                               scavenger receptor cysteine-rich protein precursor - sea urchin (Strongylocentrotus C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 11-May-2000 C;Accession: T17405
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R;Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P. Hear. Res. 130, 62-74, 1999

A;Title: Chick alpha tectorin: molecular cloning and express A;Reference number: Z20783; MUID:99251817

A;Accession: T30243
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C;Species: Gallus gallus (chicken)
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
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A;Molecule type: mRNA
A;Residues: 1-1036 <PAN>
A;Cross-references: EMBL:AF076513; NID:g4164530; PID:g4164531; PIDN:AAD05493.1
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A;Molecule type: mRNA
A;Residues: 1-2120 <COU>
A;Cross-references: EMBL:AJ012287; NID:e1361091; PID:e1361092; PIDN:CAA09979.1
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555 GDHHCPEGMTFNECGSGCGPGSCDNLVPRDICPLFCFVGCFCPEGLVKDQDGGDRCIPVD 614
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                                           GRGKCPSNEIFSRCDGRC-QRFCPNVVPKPLCIKICAPGCVCRLGYLRNKK--KVCVPRS 64
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20; Conservative
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Pred. No. 0.038;
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A; Description: The sequence A; Reference number: Z20043
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A; Accession: T30257
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R;Tomasetto, C.; Mas
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C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
                                       Qy
                                                                                    В
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A;Introns: 13/3; 84/1; 133/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C04E6.12
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A; Residues: 1-192 <BEN>
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A; Residues: 1-1023 <TOM>
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В
                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: T25513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Bentley, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: C04E6.12
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
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Best Local :
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144 TGLARNAEGKCVTLREC
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                                          50
                                                                                    88 CSKTEIYHCLD--CEPTCHNLIPK--CRKVRRTFATVFTIRDTRVQRSVQEQCNKGCVCK 143
                                                                                                                                 12 CPSNEIFSRCDGRCQRFCPNVVPKPLCIKI-----
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                                                                                                                                                                                                Similarity
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                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL:U97012; PIDN:AAB52332.1; GSPDB:GN00023; CESP:C04E6.12
e: strain Bristol N2; clone C04E6
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                                                                                                                                                                                                  Score 93; DB 2;
Pred. No. 0.024;
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Job time: 210 sec

June 21,

2001, 10:51:02

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1: 'sp_archea:*
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Gapop 10.0 , Gapext 0.5
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415.391 Million cell updates/sec
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sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                      sp_phage:*
sp_plant:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Q16938 ancylostoma			Q18157 caenorhabdi		Q9y6r7 homo sapien					P90956 caenorhabdi	O	088799 mus musculu	008523 mus musculu	Q9u1t5 caenorhabdi	Q9ult6 caenorhabdi	Q19964 caenorhabdi		Description	

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22.5	22.6	22.6	22.6	22.6	22.6	22.6	22.9	23.0	23.0	23.0	23.1	23.3	23.3	23.3	23.5	23.5	23.5	23.7	23.7	23.8	23.8	24.2	24.7	24.7	24.9
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ALIGNMENTS

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Nature 368:32-38(1994). NATURE 368:32-38(1994). EMBL; Z74031; CAA98455.1; HSSP; P56682; 1CCV. InterPro; IPR000561; InterPro; IPR002919; Pfam; PF01826; TIL; 1. PROSITE; PS01186; EGF_2; UNKNOWN_1. SEQUENCE 245 AA; 27785 MW; 781AEA77F9FE784C CRC64;	Faisons J., Fercy C., Kliken L., Koopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaudhan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398; Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,	(1) SEQUENCE FROM N.A. WILKINSON J.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.	F32D8.3. Caenorhabditis elegans. Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;	01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NAY-2000 (TrEMBLrel. 13, Last annotation update) F32D8.3 PROTEIN.	ULT 1 964 1964 PRELIMINARY; PRT; 245 AA. 019664:

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Science 282:2012-2018(1998).
EMBL; 298877; CAB54472.1; -.
HSSP; P56682; 1CCV.
InterPro; IPR000561; -.
InterPro; IPR002919; -.
Pfam; PF01826; TIL; 3.
PROSITE; PS01186; EGF_2; UNKNO
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Q9U1T5;
Q9U1T5;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2001 (TrEMBLrel. 13, L
01-MAR-2001 (TrEMBLrel. 16, L
Y69H2.3B PROTEIN.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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Submitted (AUG-1997)
                                                McMurray A.A.
                                                                   SEQUENCE FROM N.A.
                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                         Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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PS01186; EGF_2; UNKNOWN_3
561 AA; 60751 MW; 469
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RESULT
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InterPro; IPR000561; -.
InterPro; IPR001507; -.
InterPro; IPR001846; -.
InterPro; IPR002919; -.
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Interpro; IPR002919; -.
Pfam; PF01826; TIL; 4.
PROSITE; PS01186; EGF 2; UNKNOWN_3
SEQUENCE 626 AA; 67881 MW; A171
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Science 282:2012-2018(1998).
EMBL; Z98877; CAB54473.1; -.
HSSP; P56682; ICCV.
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                                                                                           PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS01286; PA58C_2; UNKNOWN_1.
PROSITE; PS01286; PA58C_2; UNKNOWN_1.
SMART; SMO0001; EGF_Like; 1.
EGF-Like domain; EGF_Like; 1.
EGF-Like domain; EGF_Like; 1.
EGF-Like domain; EGF_Like; 1.
EGF-Like domain; EGF_Like; 1.
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"The mouse tectorins. Modular matrix proteins of the inner e
homologous to components of the sperm-egg adhesion system.";
J. Biol. Chem. 272.8791-8801(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                      EMBL; X99805;
HSSP; P56682;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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 11
  KCPSNEIFSRCDGRCQRFCPNVVPKPLCIKICAPGCVCRLGYLRNKKKVCVPRSKCG
                                                                                                                                                                                     PF00094; vwd; 4.
PF00100; zona_pellucida;
PF01826; TIL; 3.
                                        Similarity
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Pred. No. 1.8e-06;
11; Mismatches 23
                            Score 113; DB Pred. No. 2.1e 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                         e 113; DB 11; .
No. 2.1e-05;
                                                                                            86C5C09AA392B1C5
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                                                                                               CRC64;
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ECPENSHFEEC-MTCTETCETLALGPICVDSCSEGCQCDEGY-RLQGSQCVTRSECG

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InterPro; 1FR003326,
InterPro; IPR003326,
InterPro; IPR0003326,
InterPro; IPR0003326,
InterPro; IPR000326,
InterPro; IPR00024; Interpro; Int
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Best Local
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O1-JAN-1998 (TrEMBLrel. 05,
O1-JAN-1998 (TrEMBLrel. 05,
O1-MAY-2000 (TrEMBLrel. 13,
                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
Wilson R., Ainscough R., Anderson
Bonfield J., Burton J., Connell M
                                                                                                                                                         Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                 Caenorhabditis elegans
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01-NOV-1998
01-NOV-1998
01-MAR-2001
                                                                                                                                         NCBI_TaxID=6239;
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EMBL; U97068; AAC26680...
InterPro; IPR000561; -.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR001846; -.
InterPro; IPR002919; -.
InterPro; IPR003328; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diversity in the structure of zonadhesin, protein containing multiple cell adhesion
                Ainscough R., Anderson K., Burton J., Connell M.,
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                       Nematoda; Chromadorea; rinae; Caenorhabditis.
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Last sequ
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Pred. No. 4.6e-05;
8; Mismatches 22;
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Sciurognathi; Muridae; Murinae; Mus
M., Copsey
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              Baynes C.
Copsey T.,
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              Cooper J., Coulson
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RESULT
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Best Local
                                               -:- SIMILARITY: BELONGS TO EMBL; Z81110; CAB03250.1; -- EMBL; Z81110; CAB03259.1; -- HSSP; P56682; ICCV InterPro; IPR000716; -- InterPro; IPR000716; --
                                                                                                                Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

-: FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).

-: CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2)

(BY SIMILARITY).
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01-AUG-1998 (TrEMBLrel. 07,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                             Caenorhabditis elegans.
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T01D3.3.
InterPro; IPR(
Pfam; PF00080;
                       InterPro;
                                     InterPro; IPR001424;
                                                                                                                                                                                   Steward
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                           NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                            P90956
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EMBL; AF016450; AAB6
HSSP; P56682; 1CCV.
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STRAIN-BRISTOL N2;
Blanchard M., Bradshaw H.;
Submitted (AUG-1997) to th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01026; TIL; 2.

TE; PS01186; EGF_2; UNKNOWN_2.

NCE 166 AA; 17971 MW; DA9;
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                       IPR002221;
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 111.5;
Pred. No. 3.6e
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DA92F2473442ADBD CRC64;
                                                                                                     SUPEROXIDE
                                                                                                                                                                                                                                                                                                                                                        949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6e-06;
nes 25;
                                                                                                                                                                                                                                                Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                  DISMUTASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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RESULT
Q9U5D0
ID Q9
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                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                           Matches
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O1-NOV-1999 (TrEMBLrel. 12, CO1-NOV-1999 (TrEMBLrel. 12, LO1-MAR-2001 (TrEMBLrel. 16, LO1-MAR-2001 (FRAGMENT).
                                                                                                                                                                                                                                                       Pfam; PF00094; vwd; 4.
Pfam; PF00629; MAM; 3.
Pfam; PF001826; TIL; 4.
Pfam; PF02345; TILa; 4.
Pfam; PF02345; TILa; 4.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS001166; EGF 2; UNKNOWN_3.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS00740; MAM_2; 6.
SMART; SM00216; VWD; 1.
SMART; SM00216; VWD; 1.
SMART; SM00216; VWD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00086; thyroglobulin_1; 1.
Pfam; PF01826; TIL; 6.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
SMART; SM00211; TY; 1.
Alternative splicing; Copper; Oxidoreductase; Zinc.
SEQUENCE 949 AA; 103486 MW; C850B2886C98E5F5 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Large scale analysis of two regions in human chromosome 7q22: annotation of 650 kb of genomic sequence around the PCOLCE and loci reveals 17 genes."; but the EMBL/GenBank/DDBJ databases.

EMBL: AF053356; AAC78790.1;
 Q9U5D0
                                                                                                                      2173 ECPAYSSYTNCLPSCSPSCWDLDGRCE---GAKVP-----SACAEGCICQPGYVLSEDK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                 2224 CVPRSQCG 2231
                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsui L.-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 CGANEQYSACFSSCQPSCQD-PSTPACPAPGCQPGCICLPGYIRRDSSPRSACVPRGLC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 CPSNEIFSRCDGRCQRFCPNVVPKPLC-IKICAPGCVCRLGYLR---NKKKVCVPRSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 loeckner G., Rosenthal A., Scherer S.,
                                                                                             60 CVPRSKCG 67
                                                                                                                                               11 KCPSNEIFSRC------DGRCQRFCPNVVPKPLCIKICAPGCVCRLGYLRNKKKV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                           9
                                                                                                                                                                           24;
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                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                        ; IPRO00561; -.
; IPRO00998; -.
; IPRO01846; -.
; IPR002919; -.
; IPR002965; -.
; IPR003328; -.
                                                                                                                                                                                                                                             2379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                           Conservative
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.0%;
                                                                                                                                                                                         27.9%;
                                                                                                                                                                                                                                               257820 MW;
                                                                                                                                                                             11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 109.5; DB 5
Pred. No. 2.8e-05;
7; Mismatches 24
                                                                                                                                                                                         Score 109; DB 4
Pred. No. 7e-05;
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C850B2886C98E5F5 CRC64;
                                                                                                                                                                                                                                               690D092316CEC94D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2379 AA
     3843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weber
                                                                                                                                                                                                      DB_4; Length 2379;
      A
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                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 949;
                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUTL1
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                                                                                                                                                                                Gaps
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FlyBase; FBgn0029167; Hml.
InterPro; IPR000359; ...
InterPro; IPR000421; ...
InterPro; IPR000436; ...
InterPro; IPR000561; ...
R InterPro; IPR001007; ...
R InterPro; IPR001092; ...
R InterPro; IPR001946; ...
JR InterPro; IPR001846; ...
JR InterPro; IPR001846; ...
JR InterPro; IPR002919; ...
InterPro; IPR002919; ...
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01185; CTCK_1; UNKNOWN_1.
PROSITE; PS01125; CTCK_2; 1.
PROSITE; PS01022; EGF_1; UNKNOWN_2.
PROSITE; PS010186; EGF_2; UNKNOWN_1.
PROSITE; PS01186; EA58C_2; UNKNOWN_1.
PROSITE; PS01086; LDLRA_2; 1.
PROSITE; PS01008; LDLRA_2; 1.
PROSITE; PS01208; LWFC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Goto A., Kumagai C., Kumagai T., Hirose J., Narit
Mori H., Kadowaki T., Kitagawa Y.;
"Identification and cloning of Hemolectin : A Dro
homology to the silkworm hemocytin and mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9U5DO;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEMOLECTIN.
                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                            1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HML OR CG7002
SEQUENCE FROM N.A
                                        Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                        Q9VU94;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00032; CCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor.
                          Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                   Drosophila melanogaster (Fruit fly)
                                                                                                                 HML PROTEIN
                                                                                                                                                                                     Q9VU94
                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein
                                                                                                  HML OR CG7002
                                                                                                                                                                                                                                                                                     11 KCPSNEIFSRCDGRCQRFCPNVVPKPLCIKICAPGCVCRLGYLRNKKKVCVPRSKC 66
                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LDLRA) DOMAIN
                                                                                                                                                                                                                                                          KCPLGQVFDECGDGCALSCDDLPSKGSCKRECVEGCRCPHGEYVNEDGECVPKKMC 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00094; vwd; 5.
PF00754; F5_F8_type_C; 2.
PF01826; TIL; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB035891;
                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                         3843 AA; 426349 MW;
                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAA88518.1; -.
                                                                                                                                                                                                                                                                                                                                27.6%;
33.9%;
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Last annotation update)
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                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                  Score 108; DB 5;
Pred. No. 0.00014;
                                                                                                                                                                                        PRT;
                                                                       Tracheata; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                          20095BC3BF21E49D CRC64;
                                                                                                                                                                                          3843 AA.
                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Narita
                                                                                                                                                                                                                                                                                                                       30;
                                                           Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila
                                                                                                                                                                                                                                                                                                                                                 Length 3843;
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                                                                                                                                                                                                                                                                                                                       Indels
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                                                                            Insecta;
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                                                             Muscomorpha;
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RA Ballew R.M., Basu A., Baxendale J. Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Hogwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodsge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong Y., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong G., Stapleton M., Strong G., Zhao Q., Zheng L.,
RA Zheng X.H., Wang S., Wang S., Zhu X., Smith H.O.,
RA Zheng R.H., Wang S., Wang S., Zhu X., Smith H.O.,
RA Zheng R.H., W
                                                                                                                                  Matches
                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0029167; Hml.
InterPro; IPR000359; -.
InterPro; IPR000421; -.
InterPro; IPR000561; -.
InterPro; IPR001007; -.
InterPro; IPR001107; -.
InterPro; IPR0012172; -.
InterPro; IPR0022172; -.
InterPro; IPR002319; -.
Pfam; PF00094; VMd; 10.
Pfam; PF00094; F5_FB_ttye_C; 4.
Pfam; PF00754; F5_FB_ttye_C; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
          1130
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
The Company of the Compa
                                                                                                                                                                                                                                                                                    Glycoprotein.
SEQUENCE 3843 AA; 426241 MW; 78D770C0B8B6319D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
                                                               11 KCPSNEIFSRCDGRCQRFCPNVVPKPLCIKICAPGCVCRLGYLRNKKKVCVPRSKC
                                                                                                                                                                Local Similarity
KCPLGQVFDECGDGCALSCDDLPSKGSCKRECVEGCRCPHGEYVNEDGECVPKKMC 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P56682; 1CCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE003536;
                                                                                                                                                                                                                                                                                                                                                       PS01208; VWFC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01185; CTCK_1; UNKNOWN_1
PS01225; CTCK_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                            PS50068;
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF49795.2;
                                                                                                                                                                                                                                                                                                                                                                                  ; EGF_1; UNKNOWN_2.
; EGF_2; UNKNOWN_1.
; FA58C_2; UNKNOWN_1.
; LDLRA_2; 1.
                                                                                                                                                            27.6%;
                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1.
                                                                                                                           Score 108; DB; Pred. No. 0.00
                                                                                                                                                            DB 5;
                                                                                                                                                                                          Length 3843;
                                                                                                                              Indels
                                                                                                                              0;
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В Q

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983 ECPENSHFEECI-TCTETCETLTLGPICVDSCSEGCQCDEGYALLGSQ-CVTRSECG 11 KCPSNEIFSRCDGRCQRFCPNVVPKPLCIKICAPGCVCRLGYLRNKKKVCVPRSKCG

1037

۷,

Matches

Similarity

Conservative

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O75443
ID 075443
ID 075443
ID 077 011
DT 011
DT 011
DT 011
DT 011
DT 011
DT 011
RR RR SERIM
OC ELLI
OC MELLI
OC
                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF055125

EMBL; AF055126

EMBL; AF055128

EMBL; AF055129

EMBL; AF055130

EMBL; AF055131

EMBL; AF055131

EMBL; AF055133

EMBL; AF055133

EMBL; AF055133

EMBL; AF055133

EMBL; AF055134

EMBL; AF055135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF055119; AAC26019
EMBL; AF055120; AAC26019
EMBL; AF055121; AAC26019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                  PROSITE: PS01186; EGF_2; 3.

PROSITE: PS01286; FA58C_2; UNKNOWN_1.

PROSITE: PS00682; ZP_DOMAIN; 1.

SMART; SM00001; EGF_11ke; 1.
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000421; -.
InterPro; IPR000561; -.
InterPro; IPR001507; -.
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EMBL; AF055123; AAC2601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF055116; AAC2601
EMBL; AF055117; AAC2601
EMBL; AF055118; AAC2601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 19:60-62(1990
EMBL; AF055136; AAC26019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Govaerts P.J., Van Camp G.;
"Mutations in the human alpha-tectorin gene cause autosomal dominant non-syndromic hearing impairment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schatteman I.,
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001846; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF055115; AAC260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richardson G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98250172; Pubme
Verhoeven K., Van Laer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPHA-TECTORIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith R.J.H., Somers T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF055125;
AF055126;
AF055127;
AF055128;
                                                                                                                                                                                                                                                                   PF00100; zona_pellucida; PF01826; TIL; 3.
                                                                                                                                                                                                                                                                                                                   PF00094; vwd; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF055135;
                                                                                                                                           domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                               IPR002919; -.
                                                                                                                          2155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19:60-62(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /an Laer L., Kirschhofer K., Legan P.K., Hughes D.C.,
Verstreken M., Van Hauwe P., Coucke P., Chen A.,
Somers T., Offeciers F.E., Van de Heyning P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC26019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC26019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wachtler F., Kimberling W.J., Willems P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=9590290;
                      27.4%;
                                                                                                                          239425
                                                                                                                       , WM
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Score 107; DB 4;
Pred. No. 0.00011;
7; Mismatches 27
                                                                                                                       54EA8B12AE3690C9 CRC64;
                                             Length 2155;
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RESULT QPY6R7
ID 67
ID 67
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ID 70
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Best Local Similarity
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Q9U1U6;
01-MAY-2000 (TIEN
01-MAY-2000 (TIEN
01-MAR-2001 (TIEN
Y69H2.4 PROTEIN.
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Q9Y6R7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arellano A., Sanders C., Ow Olsen A.S., Carrano A.V.; "Sequence analysis of a 2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999
01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene.
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                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00858; MTCRUSTACEAN. PROSITE; PS01186; EGF_2; 6. SMART; SM00274; FOLN; 1.
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF-like domain; Glycoprotein.
NON_TER 2843 2843
                                         MEDLINE=99069613;
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                   Submitted
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amerdin J.E., McCready P.M., Richardson P., Sakaldasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 KCPSNEIFSRCDGRCQRFCPNVVPKPLCIKICAPGCVCRLGYLRNKKKVCVPRSKCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF010094; .vwd; 6. PF01826; TIL; 6.
                                                                                                                                                   (AUG-1997)
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(TrEMBLrel. 13, 
(TrEMBLrel. 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     Peloderinae;
                                         PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                     Caenorhabditis
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Last sequence update)
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Pred. No. 0.00017;
6; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Scott D., Skowronski E.,
                                                                                                                                                                                                                                                                                                                                                                           Rhabditida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology,";
Science 28:2012-2018(1998).
Science 28:2012-2018(1998).
EMBL; Z98877; CAB63401.1; -.
InterPro; IPR000561; -.
InterPro; IPR002919; -.
Pfam; PF01826; TIL; 4.
PROSITE; PS01186; EGF-2; UNKNOWN_3.
SEQUENCE 453 AA; 47861 MW; FD4CC
InterPro; IPRO00561; -.
InterPro; IPRO02919; -.
Pfam; PF01826; TIL; -.
PROSITE; PS01186; EGF_2; 2.
EGF-like domain; Glycoprotein.
SEQUENCE 137 AA; 14948 MW; 3
                                                                                                                                                                                                                                                                                                        Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulsor
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston I.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Riften L., Roopra A., Saunders D., Shownkee
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Cr
01-NOV-1996 (TrEMBLrel. 01, La
01-NOV-1996 (TrEMBLrel. 16, La
01-MAR-2001 (TrEMBLrel. 16, La
SIMILARITY TO EGF-LIKE DOMAIN
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Q18157;
                                                                                                                                                                                                                                                                                       Watson A., Weinstock D., ... "2.2 Mb of contiguous nucleotide alegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                             Submitted (FEB-1996) to the EMBL; U50311; AAA92313.1; -. HSSP; P56682; ICCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C.elegans: A platform for
investigating biology.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                             Waterston R.;
                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                       Bradshaw H
                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYSTEINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FD4CC2A42CDB8DC4 CRC64;
        35A3763760F88E30 CRC64;
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                                                                                                                                                                                                                                                                                                                                   Query Match 25.7
Best Local Similarity 37.3
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000561; -. InterPro; IPR002919; -. Pfam; PF01826; TIL; 3. PROSITE; PS01186; EGF_2; UNKNOWN_2. SEQUENCE 211 AA; 22393 MW; 95D23AB9353389A7 CRC64;
                                                                                                                                                         investigating biology, ";
Science 282:2012-2018(1998).
EMBL; Z98877; CAB63407.1; -.
HSSP; P19398; 1ATB.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Q9U1U0;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y69H2.10 PROTEIN.
Y69H2.10.
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                                                                                                                                                                                                                                                                                                                   25.7%; Score 100.5; DB 5; Length 211; 37.3%; Pred. No. 9.6e-05; ative 8; Mismatches 26; Indels 3; Gaps
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